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<110> E. I. du Pont de Nemours and Company  
Pioneer Hi-Bred International, Inc.

<120> Auxin Transport Proteins

<130> BB1355

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<150> 60/133,040

<151> 1999-05-07

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Ile Gly Val Val Trp Ser Leu Val Ser Tyr Arg Trp Gly Ile Glu Met  
 35 40 45

Pro Ala Ile Ile Ala Arg Ser Ile Ser Ile Leu Ser Asp Ala Gly Leu  
 50 55 60

Gly Met Ala Met Phe Ser Leu Gly Leu Phe Met Ala Leu Gln Pro Arg  
 65 70 75 80

Ile Ile Ala Cys Gly Asn Lys Leu Ala Ala Ile Ala Met Gly Val Arg  
 85 90 95

Phe Val Ala Gly Pro Ala Val Met Ala Ala Ala Ser Ile Ala Val Gly  
 100 105 110

Leu Arg Gly Val Leu Leu His Ile Ala Ile Val Gln Ala Ala Leu Pro  
 115 120 125

Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Gly Val His Pro  
 130 135 140

Asp Ile Leu Ser Thr Ala Val Ile Phe Gly Met Leu Ile Ala Leu Pro  
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Ile Thr Leu Val Tyr Tyr Ile Leu Leu Gly Leu  
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 35 40 45

Ile Gly Val Ile Trp Ser Leu Val Cys Phe Arg Trp Asn Phe Gln Met  
 50 55 60

Pro Ala Ile Val Leu Gln Ser Ile Ser Ile Leu Ser Asp Ala Gly Leu  
 65 70 75 80

Gly Met Ala Met Phe Ser Leu Gly Leu Phe Met Ala Leu Gln Pro Arg  
 85 90 95

Ile Ile Ala Cys Gly Asn Lys Val Ala Thr Phe Ala Met Ala Val Arg  
 100 105 110

Phe Leu Thr Gly Pro Ala Val Met Ala Ala Ser Phe Ala Val Gly  
 115 120 125

Leu Arg Gly Thr Leu Leu His Val Ala Ile Val Gln Ala Ala Leu Pro  
 130 135 140

Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Val His Pro  
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Asp Ile Leu Ser Thr Ala Val Ile Phe Gly Met Leu Ile Ala Leu Pro  
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Ile Thr Leu Val Tyr Tyr Ile Leu Leu Gly Leu  
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tcgatcgca agatgatcac cggcacggan cttctaccac gtcntgacgg ccatggtgcc 180  
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35 40 45  
Phe Xaa Val Pro Leu Leu Ser Phe His Phe Ile Ser Xaa Gln Gln Pro  
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Tyr Thr Met Asn Leu Arg Phe Ile Ala Ala Glu Thr Trp Gln  
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<213> Zea mays

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 35 40 45  
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asn Pro  
 50 55 60  
 Tyr Thr Met Asn Leu Arg Phe Ile Ala Ala Asp Thr Leu Gln Lys Leu  
 65 70 75 80  
 Met Val Leu Ala Met Leu Thr Ala Trp Ser His Leu Ser Arg Arg Gly  
 85 90 95  
 Ser Leu Glu Trp Thr Ile Thr Leu Phe Ser Leu Ser Thr Leu Pro Asn  
 100 105 110  
 Thr Leu Val Met Gly Ile Pro Leu Leu Lys Gly Met Tyr Gly Asp Phe  
 115 120 125

Ser Gly Ser Leu Met Val Gln Ile Val Val Leu Gln Cys Ile Ile Trp  
130 135 140

Tyr Thr Leu Met Leu Phe Met Phe Glu Tyr Arg Gly Ala Arg Met Leu  
145 150 155 160

Ile Thr Glu Gln Phe Pro Asp Asn Ala Gly Ala Ile Ala Ser Ile Val  
165 170 175

Val Asp Pro Asp Val Val Ser Leu Asp Gly Arg Arg Asp Ala Ile Glu  
180 185 190

Thr Glu Ala Glu Val Lys Glu Asp Gly Arg Ile His Val Thr Val Arg  
195 200 205

Arg Ser Asn Ala Ser Arg Ser Asp Ile Tyr Ser Arg Arg Ser Met Gly  
210 215 220

Phe Ser Ser Thr Thr Pro Arg Pro Ser Asn Leu Thr Asn Ala Glu Ile  
225 230 235 240

Tyr Ser Leu Gln Ser Ser Arg Asn Pro Thr Pro Arg Gly Ser Ser Phe  
245 250 255

Asn His Asn Asp Phe Tyr Ser Met Val Gly Arg Ser Ser Asn Phe Gly  
260 265 270

Ala Ala Asp Ala Phe Gly Ile Arg Thr Gly Ala Thr Pro Arg Pro Ser  
275 280 285

Asn Tyr Glu Asp Asp Ala Ser Lys Pro Lys Tyr Pro Leu Pro Val Val  
290 295 300

Asn Ala Thr Ser Gly Ala Gly Ala Ala His Tyr Pro Ala Pro Asn Pro  
305 310 315 320

Ala Val Ala Ala Ala Pro Lys Gly Ala Arg Lys Ala Ala Thr Asn Gly  
325 330 335

Gln Ala Lys Gly Glu Asp Leu His Met Phe Val Trp Ser Ser Ala  
340 345 350

Ser Pro Val Ser Asp Val Phe Gly Gly Ala Pro Asp Tyr Asn Glu  
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 Xaa Xaa Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Leu  
 35 40 45  
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asp Pro  
 50 55 60  
 Phe Ala Met Asn Leu Arg Phe Leu Ala Val Asp Thr Leu Gln Lys Val  
 65 70 75 80  
 Ala Val Leu Ala Leu Leu Ala Leu Xaa Ser Xaa Ala Ala Ser Ser Xaa  
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 Arg Xaa Arg Ser Gly Leu Asp Trp Ser Ile Lys Leu Xaa Xaa Leu Ser  
 100 105 110  
 Thr Leu

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 <212> DNA  
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 aaaaaaaaaag 2769

&lt;210&gt; 14

&lt;211&gt; 573

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;400&gt; 14

Met	Ile	Thr	Ala	Leu	Asp	Leu	Tyr	His	Val	Leu	Thr	Ala	Val	Val	Pro
1				5					10				15		

Leu	Tyr	Val	Ala	Met	Thr	Leu	Ala	Tyr	Gly	Ser	Val	Arg	Trp	Trp	Arg
				20				25				30			

Ile	Phe	Thr	Pro	Asp	Gln	Cys	Ser	Gly	Ile	Asn	Arg	Phe	Val	Ala	Leu
					35			40				45			

Phe	Ala	Val	Pro	Leu	Leu	Ser	Phe	His	Phe	Ile	Ser	Thr	Asn	Asp	Pro
					50			55				60			

Phe	Ala	Met	Asn	Leu	Arg	Phe	Leu	Ala	Ala	Asp	Thr	Leu	Gln	Lys	Val
				65			70			75			80		

Ala	Val	Leu	Ala	Leu	Leu	Ala	Leu	Ala	Ser	Arg	Gly	Leu	Ser	Ser	Pro
					85				90				95		

Arg	Ala	Leu	Gly	Leu	Asp	Trp	Ser	Ile	Thr	Leu	Phe	Ser	Leu	Ser	Thr
					100				105			110			

Leu	Pro	Asn	Thr	Leu	Val	Met	Gly	Ile	Pro	Leu	Leu	Arg	Gly	Met	Tyr
					115				120			125			

Gly	Ala	Ser	Ser	Ala	Gly	Thr	Leu	Met	Val	Gln	Val	Val	Val	Leu	Gln
					130			135			140				

Cys	Ile	Ile	Trp	Tyr	Thr	Leu	Met	Leu	Phe	Leu	Phe	Glu	Tyr	Arg	Ala
						145		150			155			160	

Ala Arg Ala Leu Val Leu Asp Gln Phe Pro Asp Gly Ala Ala Ala Ser  
165 170 175

Ile Val Ser Phe Arg Val Asp Ser Asp Val Val Ser Leu Ala Arg Gly  
180 185 190

Asp Val Glu Leu Glu Ala Glu Pro Asp Gly Val Ala Gly Ala Gly Ala  
195 200 205

Val Ser Ser Arg Gly Gly Asp Ala Gly Arg Val Arg Val Thr Val Arg  
210 215 220

Lys Ser Thr Ser Ser Arg Ser Glu Ala Ala Cys Ser His Ser His Ser  
225 230 235 240

Gln Thr Met Gln Pro Arg Val Ser Asn Leu Ser Gly Val Glu Ile Tyr  
245 250 255

Ser Leu Gln Ser Ser Arg Asn Pro Thr Pro Arg Gly Ser Ser Phe Asn  
260 265 270

His Ala Asp Phe Phe Asn Ile Val Gly Ala Ala Ala Lys Gly Gly Gly  
275 280 285

Gly Ala Ala Gly Asp Glu Glu Lys Gly Ala Cys Gly Gly Gly Gly  
290 295 300

Gly His Ser Pro Gln Pro Gln Ala Val Ala Val Pro Ala Lys Arg Lys  
305 310 315 320

Asp Leu His Met Leu Val Trp Ser Ser Ser Ala Ser Pro Val Ser Glu  
325 330 335

Arg Ala Ala Val His Val Phe Gly Ala Gly Gly Ala Asp His Ala Asp  
340 345 350

Val Leu Ala Lys Gly Ala Gln Ala Tyr Asp Glu Tyr Gly Arg Asp Asp  
355 360 365

Tyr Ser Ser Arg Thr Lys Asn Gly Ser Gly Gly Ala Asp Lys Gly Gly  
370 375 380

Pro Thr Leu Ser Lys Leu Gly Ser Asn Ser Thr Ala Gln Leu Tyr Pro  
385 390 395 400

Lys Asp Asp Gly Glu Gly Arg Ala Ala Ala Val Ala Met Pro Pro Ala  
405 410 415

Ser Val Met Thr Arg Leu Ile Leu Ile Met Val Trp Arg Lys Leu Ile  
420 425 430

Arg Asn Pro Asn Thr Tyr Ser Ser Leu Ile Gly Val Val Trp Ser Leu  
435 440 445

Val Ser Tyr Arg Trp Gly Ile Glu Met Pro Ala Ile Ile Ala Arg Ser  
450 455 460

Ile Ser Ile Leu Ser Asp Ala Gly Leu Gly Met Ala Met Phe Ser Leu  
465 470 475 480

Gly Leu Phe Met Ala Leu Gln Pro Arg Ile Ile Ala Cys Gly Asn Lys  
485 490 495

Leu Ala Ala Ile Ala Met Gly Val Arg Phe Val Ala Gly Pro Ala Val  
500 505 510

Met Ala Ala Ala Ser Ile Ala Val Gly Leu Arg Gly Val Leu Leu His  
515 520 525

Ile Ala Ile Val Gln Ala Ala Leu Pro Gln Gly Ile Val Pro Phe Val  
530 535 540

Phe Ala Lys Glu Tyr Gly Val His Pro Asp Ile Leu Ser Thr Ala Tyr  
545 550 555 560

Gly Pro Ile Thr Ser His Gly Phe Ile Thr Cys His Ser  
565 570

<210> 15  
<211> 543  
<212> DNA  
<213> Oryza sativa

<220>  
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<222> (42)

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tgtacgccag cgttctcgcc gtcgtgtggg cgtgcacatcg cgtacaggtgg cacctgagct 180  
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ccgcccctt cgggnctccgc ggcgacgtcc tgcacctcg ccatcatacag gncgnactgc 420  
tcaatcgatt nttcttcgtt ttncaaagga gtatggctta ttncatgac tcagnacggc 480  
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atn 543

<210> 16  
<211> 110  
<212> PRT  
<213> Oryza sativa

<220>  
<221> UNSURE  
<222> (108)..(109)

<400> 16  
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Gly Val Val Trp Ala Cys Ile Ala Tyr Arg Trp His Leu Ser Leu Pro  
20 25 30

Gly Ile Val Thr Gly Ser Leu Gln Val Met Ser Arg Thr Gly Thr Gly  
35 40 45

Met Ser Met Phe Ser Met Gly Leu Phe Met Gly Gln Gln Glu Arg Val  
 50 55 60

Ile Ala Cys Gly Ala Gly Leu Thr Ala Leu Gly Met Ala Leu Arg Phe  
 65 70 75 80

Val Ala Gly Pro Leu Ala Thr Leu Val Gly Ala Ala Ala Leu Gly Leu  
 85 90 95

Arg Gly Asp Val Leu His Leu Ala Ile Ile Gln Xaa Xaa Leu  
 100 105 110

<210> 17

<211> 330

<212> DNA

<213> Oryza sativa

<400> 17

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 acacgggtat ggccggcggtg gtggcgtgt acgtggcgat gttcctggcg tacgggtcgg 180  
 tgcgggtgtg gggcatcttc acggccggacc agtgctccgg catcaaccgc ttcgtcgcca 240  
 tcttcggcgtt gcccgtcctg tccttccact tcatctccac caacgaccgg tacggcatga 300  
 acctccgctt cctggcgccg ggacacgctg 330

<210> 18

<211> 74

<212> PRT

<213> Oryza sativa

<400> 18

Met Ile Ser Gly His Asp Phe Tyr Thr Val Met Ala Ala Val Val Pro  
 1 5 10 15

Leu Tyr Val Ala Met Phe Leu Ala Tyr Gly Ser Val Arg Trp Trp Gly  
 20 25 30

Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Ile  
 35 40 45

Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asp Pro  
 50 55 60

Tyr Ala Met Asn Leu Arg Phe Leu Ala Ala  
 65 70

<210> 19

<211> 2162

<212> DNA

<213> Oryza sativa

<400> 19

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 acacgggtat ggccggcggtg gtggcgtgt acgtggcgat gttcctggcg tacgggtcgg 180  
 tgcgggtgtg gggcatcttc acggccggacc agtgctccgg catcaaccgc ttcgtcgcca 240  
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 acctccgctt cctggcgccg gacacgctg agaagctgt cgtcctggcg gggctcgccg 360  
 cgtggtcgg cctccctcg cggaccggccg cgccgcggct ggactggtcc atcacgctct 420  
 tctccctctc cacgctgccc aacacgctg tcatggggat cccgctgctg atcgccatgt 480

acgggccata	ctccggctcg	ctcatggtcc	agatcgtcgt	gctccagtgc	atcatctgg	540
acacgctgat	gctcttcctc	ttcgagttcc	gcgcgcgcgc	gatgctgatc	gcccggccgt	600
tcccggacac	ggcggcggtcc	atcggttccc	tgcacgtcga	cccgacgtg	gtgtcgctgg	660
agggcggcca	cgcggagacg	gaggccgagg	tggccgggaa	cggccggctg	cacgtcaccg	720
tgcggcggtc	ctcggtgtcg	cggcggtcgc	tgctggtcac	gccgcggccg	tcgaacctga	780
cgggagcgg	gatctactcg	cttagctcg	cgcggaaaccc	aaccccgccg	ggctccaact	840
tcaaccacgc	cgacttcttc	gcatggtgcg	gcggcgggccc	accggcccc	acgcccgtg	900
cggtgccgg	ctcgagcttc	ggccctccg	agctttaactc	gtcgaatcg	tcgcggggcc	960
caaccccgag	gcagtccaaac	ttcgacgagc	actcggcacg	gccgcggaaa	ccacccggcaa	1020
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cttccggat	tgttcatggc	gtcgcagccc	agcatcatcg	cgtgtggcaa	atcagccgccc	1620
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ggactatgtat	caagaaagct	tatggacgct	ctcacataaa	acggaagaaa	tggggcaaa	1920
gagagagaaa	aaaaagcgat	cctgtccatc	tcaaacagcg	tatgcttata	tgtatagcct	1980
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aa						2162

&lt;210&gt; 20

&lt;211&gt; 589

&lt;212&gt; PRT

&lt;213&gt; Oryza sativa

&lt;400&gt; 20

Met	Ile	Ser	Gly	His	Asp	Phe	Tyr	Thr	Val	Met	Ala	Ala	Val	Val	Pro
1						5				10					15

Leu	Tyr	Val	Ala	Met	Phe	Leu	Ala	Tyr	Gly	Ser	Val	Arg	Trp	Trp	Gly
										25					30

Ile	Phe	Thr	Pro	Asp	Gln	Cys	Ser	Gly	Ile	Asn	Arg	Phe	Val	Ala	Ile
									35					40	45

Phe	Ala	Val	Pro	Leu	Leu	Ser	Phe	His	Phe	Ile	Ser	Thr	Asn	Asp	Pro
									50					55	60

Tyr	Ala	Met	Asn	Leu	Arg	Phe	Leu	Ala	Ala	Asp	Thr	Leu	Gln	Lys	Leu	
									65					70	75	80

Leu	Val	Leu	Ala	Gly	Leu	Ala	Ala	Trp	Ser	Arg	Leu	Pro	Ser	Arg	Thr
									85					90	95

Gly	Ala	Pro	Arg	Leu	Asp	Trp	Ser	Ile	Thr	Leu	Phe	Ser	Leu	Ser	Thr
								100						105	110

Leu	Pro	Asn	Thr	Leu	Val	Met	Gly	Ile	Pro	Leu	Leu	Ile	Ala	Met	Tyr
								115						120	125

Gly Pro Tyr Ser Gly Ser Leu Met Val Gln Ile Val Val Leu Gln Cys  
130 135 140

Ile Ile Trp Tyr Thr Leu Met Leu Phe Leu Phe Glu Phe Arg Ala Ala  
145 150 155 160

Arg Met Leu Ile Ala Asp Gln Phe Pro Asp Thr Ala Ala Ser Ile Val  
165 170 175

Ser Leu His Val Asp Pro Asp Val Val Ser Leu Glu Gly Gly His Ala  
180 185 190

Glu Thr Glu Ala Glu Val Ala Ala Asp Gly Arg Leu His Val Thr Val  
195 200 205

Arg Arg Ser Ser Val Ser Arg Arg Ser Leu Leu Val Thr Pro Arg Pro  
210 215 220

Ser Asn Leu Thr Gly Ala Glu Ile Tyr Ser Leu Ser Ser Ser Arg Asn  
225 230 235 240

Pro Thr Pro Arg Gly Ser Asn Phe Asn His Ala Asp Phe Phe Ala Met  
245 250 255

Val Gly Gly Pro Pro Pro Pro Thr Pro Ala Ala Val Arg Gly Ser  
260 265 270

Ser Phe Gly Ala Ser Glu Leu Tyr Ser Leu Gln Ser Ser Arg Gly Pro  
275 280 285

Thr Pro Arg Gln Ser Asn Phe Asp Glu His Ser Ala Arg Pro Pro Lys  
290 295 300

Pro Pro Ala Thr Thr Gly Ala Leu Asn His Asp Ala Lys Glu Leu  
305 310 315 320

His Met Phe Val Trp Ser Ser Ser Ala Ser Pro Val Ser Glu Val Ser  
325 330 335

Gly Leu Pro Val Phe Ser Gly Gly Gly Gly Gly Ala Leu Asp Val  
340 345 350

Gly Ala Lys Glu Ile His Met Val Ile Pro Ala Asp Leu Pro Gln Asn  
355 360 365

Asn Gly Ser Gly Lys Glu His Glu Glu Tyr Gly Ala Val Ala Leu Gly  
370 375 380

Gly Gly Gly Gly Glu Asn Phe Ser Phe Gly Gly Gly Lys Thr Val  
385 390 395 400

Asp Gly Ala Glu Ala Val Asp Glu Glu Ala Ala Leu Pro Asp Gly Leu  
405 410 415

Thr Lys Met Gly Ser Ser Ser Thr Ala Glu Leu His Pro Lys Val Val  
420 425 430

Asp Val Asp Gly Pro Asn Ala Gly Gly Ala Ala Gly Ala Gly Gln  
435 440 445

Tyr Gln Met Pro Pro Ala Ser Val Met Thr Arg Leu Ile Leu Ile Met  
 450 455 460

Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser Ser Leu Leu  
 465 470 475 480

Gly Leu Ala Trp Ser Leu Val Ala Phe Arg Leu Phe Met Ala Leu Gln  
 485 490 495

Pro Ser Ile Ile Ala Cys Gly Lys Ser Ala Ala Val Val Ser Met Ala  
 500 505 510

Val Arg Phe Leu Ala Gly Pro Ala Val Met Ala Ala Ala Ser Ile Ala  
 515 520 525

Ile Gly Leu Arg Gly Thr Leu Leu His Val Ala Ile Val Gln Ala Ala  
 530 535 540

Leu Pro Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Val  
 545 550 555 560

His Pro Ala Ile Leu Ser Thr Ala Val Ile Phe Gly Met Leu Ile Ala  
 565 570 575

Leu Pro Ile Thr Leu Leu Tyr Tyr Ile Leu Leu Gly Leu  
 580 585

<210> 21

<211> 1618

<212> DNA

<213> Glycine max

<400> 21

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 aagaggacgg caagctccac gtcactgtca gaaaatccaa cgcttccaga tccgacatct 180  
 tttctagaag gtcccaggc ttcttcca ccaccctcg cccttccaaat ctcaccaatg 240  
 ctgagattta ctctttcag tcctctcgaa accctactcc acgtggctcc agtttcaacc 300  
 acaccgattt ctactccat atggctgtcg gtcgttaattc taactttggt gccaacgatg 360  
 tttatggcct ttctgtttcc agaggaccaa ctcccagacc ttccaattac gacgaggatg 420  
 cttctaataa taacaatggg aagccgaggt accactaccc tgctgctgga acaggaacag 480  
 gaacaggaac aggaacggga acgggaacag ggcactaccc tgctcctaac cctggcatgt 540  
 tctctccac tgcttctaaa aacgtcgcca agaagccaga cgatccaaat aaggaccttc 600  
 atatgttcgt ttggagttca agtctttcc cggtttcgga tttgtttggg ggtggacatg 660  
 aatatgatca taaagaactc aagtttaactg tatctccagg aaaagtggag ggtaatatta 720  
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 ggattgagga tgagcatgaa ggtgagaaag ttggaaacgg aatccaaaa acaatgcctc 840  
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 ctcttcctt tttttttat gaattgtcct tgctcagtga aatgtaaaa tcatgtttgt 1560  
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<210> 22  
<211> 443  
<212> PRT  
<213> Glycine max

<400> 22  
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Val Asp Ser Asp Val Met Ser Leu Asp Gly Arg Gln His Pro Leu Glu  
20 25 30  
Thr Asp Ala Gln Ile Lys Glu Asp Gly Lys Leu His Val Thr Val Arg  
35 40 45  
Lys Ser Asn Ala Ser Arg Ser Asp Ile Phe Ser Arg Arg Ser Gln Gly  
50 55 60  
Phe Ser Ser Thr Thr Pro Arg Pro Ser Asn Leu Thr Asn Ala Glu Ile  
65 70 75 80  
Tyr Ser Leu Gln Ser Ser Arg Asn Pro Thr Pro Arg Gly Ser Ser Phe  
85 90 95  
Asn His Thr Asp Phe Tyr Ser Met Met Ala Ala Gly Arg Asn Ser Asn  
100 105 110  
Phe Gly Ala Asn Asp Val Tyr Gly Leu Ser Ala Ser Arg Gly Pro Thr  
115 120 125  
Pro Arg Pro Ser Asn Tyr Asp Glu Asp Ala Ser Asn Asn Asn Asn Gly  
130 135 140  
Lys Pro Arg Tyr His Tyr Pro Ala Ala Gly Thr Gly Thr Gly Thr Gly  
145 150 155 160  
Thr Gly Thr Gly Thr Gly His Tyr Pro Ala Pro Asn Pro Gly  
165 170 175  
Met Phe Ser Pro Thr Ala Ser Lys Asn Val Ala Lys Lys Pro Asp Asp  
180 185 190  
Pro Asn Lys Asp Leu His Met Phe Val Trp Ser Ser Ala Ser Pro  
195 200 205  
Val Ser Asp Val Phe Gly Gly His Glu Tyr Asp His Lys Glu Leu  
210 215 220  
Lys Leu Thr Val Ser Pro Gly Lys Val Glu Gly Asn Ile Asn Arg Asp  
225 230 235 240  
Thr Gln Glu Glu Tyr Gln Pro Glu Lys Asp Glu Phe Ser Phe Gly Asn  
245 250 255  
Arg Gly Ile Glu Asp Glu His Glu Gly Glu Lys Val Gly Asn Gly Asn  
260 265 270  
Pro Lys Thr Met Pro Pro Ala Ser Val Met Thr Arg Leu Ile Leu Ile  
275 280 285

Met Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser Ser Leu  
290 295 300

Ile Gly Leu Thr Trp Ser Leu Ile Ser Phe Arg Trp Asn Val Lys Met  
305 310 315 320

Pro Ala Ile Ile Ala Lys Ser Ile Ser Ile Leu Ser Asp Ala Gly Leu  
325 330 335

Gly Met Ala Met Phe Ser Leu Gly Leu Phe Met Ala Leu Gln Pro Arg  
340 345 350

Ile Ile Ala Cys Gly Asn Ser Thr Ala Ala Phe Ser Met Ala Val Arg  
355 360 365

Phe Leu Thr Gly Pro Ala Val Met Ala Ala Ala Ser Ile Ala Val Gly  
370 375 380

Leu Lys Gly Val Leu Leu His Val Ala Ile Val Gln Ala Ala Leu Pro  
385 390 395 400

Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Val His Pro  
405 410 415

Asp Ile Leu Ser Thr Gly Val Ile Phe Gly Met Leu Ile Ala Leu Pro  
420 425 430

Ile Thr Leu Val Tyr Tyr Ile Leu Leu Gly Leu  
435 440

<210> 23

<211> 531

<212> DNA

<213> Glycine max

<220>

<221> unsure

<222> (530)

<400> 23

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tcttcacc ggaccagtgc tccggcataa accgcttcgt ggcgatcttc gccgtgccc 420  
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<210> 24

<211> 90

<212> PRT

<213> Glycine max

<220>

<221> UNSURE

<222> (33)

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 <222> (78)

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 20 25 30  
 Xaa Ile Phe Ser Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala  
 35 40 45  
 Ile Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asn  
 50 55 60  
 Pro Tyr Ala Met Asn Phe Arg Phe Ile Arg Arg Arg Thr Xaa Thr Ser  
 65 70 75 80  
 Lys Lys Ile Ile Met Leu Phe Ala Leu Ala  
 85 90

<210> 25  
 <211> 2101  
 <212> DNA  
 <213> Glycine max

<400> 25  
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 aaccaaaatt ttccaatttag cactagttagt acagtacaaa aaactagaag agcaacccaa 180  
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 aagatcttct caccggacca gtgtccggc ataaaccgct tcgtggcgat ctgcggctg 420  
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 atgcgcgccc acaccctcca gaagatcatc atgctttcg cccttgccat ctggaccac 540  
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 a 2101

<210> 26  
 <211> 540  
 <212> PRT  
 <213> Glycine max

<400> 26  
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 20 25 30  
 Ile Phe Ser Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Ile  
 35 40 45  
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asn Pro  
 50 55 60  
 Tyr Ala Met Asn Phe Arg Phe Ile Ala Ala Asp Thr Leu Gln Lys Ile  
 65 70 75 80  
 Ile Met Leu Phe Ala Leu Ala Ile Trp Thr Asn Leu Thr Lys Thr Gly  
 85 90 95  
 Ser Leu Glu Trp Met Ile Thr Ile Phe Ser Leu Ser Thr Leu Pro Asn  
 100 105 110  
 Thr Leu Val Met Gly Ile Pro Leu Leu Ile Ala Met Tyr Gly Asp Tyr  
 115 120 125  
 Ser Gly Ser Leu Met Val Gln Val Val Val Leu Gln Cys Ile Ile Trp  
 130 135 140  
 Tyr Thr Leu Leu Leu Phe Leu Phe Glu Tyr Arg Ala Ala Lys Ile Leu  
 145 150 155 160  
 Ile Met Glu Gln Phe Pro Glu Thr Ala Ala Ser Ile Val Ser Phe Lys  
 165 170 175  
 Val Asp Ser Asp Val Val Ser Leu Asp Gly Arg Asp Phe Leu Glu Thr  
 180 185 190  
 Asp Ala Glu Val Gly Asp Asp Gly Lys Leu His Val Thr Val Arg Lys  
 195 200 205  
 Ser Asn Ala Ser Arg Arg Ser Phe Met Met Thr Pro Arg Pro Ser Asn  
 210 215 220  
 Leu Thr Gly Ala Glu Ile Tyr Ser Leu Ser Ser Ser Arg Asn Pro Thr  
 225 230 235 240  
 Pro Arg Gly Ser Asn Phe Asn His Ala Asp Phe Phe Ser Met Met Gly  
 245 250 255

Tyr Gln Pro Arg His Ser Asn Phe Thr Ala Asn Asp Leu Phe Ser Ser  
260 265 270

Arg Gly Pro Thr Pro Arg Pro Ser Asn Phe Glu Glu Pro Ser Met Pro  
275 280 285

Gln Ala Val Thr Val Ala Ser Pro Arg Phe Gly Phe Tyr Pro Ser Gln  
290 295 300

Thr Val Pro Ala Ser Tyr Pro Pro Pro Asn Pro Asp Phe Ser Ser Ala  
305 310 315 320

Thr Lys Asn Leu Lys Asn Gln Ser Gln Asn Gln Asn Pro Asn Gln Ser  
325 330 335

Gln Ser Gln Asn Ser Gln Ala Pro Ala Lys Gly Ala His Asp Ala Lys  
340 345 350

Glu Leu His Met Phe Val Trp Ser Ser Ser Ala Ser Pro Met Ser Glu  
355 360 365

Asn Ala Gly Leu Asn Val Phe Ser Ser Thr Asp Leu Gly Thr Ser Glu  
370 375 380

Gln Pro Asp Gln Gly Ala Lys Glu Ile Arg Met Leu Val Ala Asp Asn  
385 390 395 400

Asn Ala His Leu Arg Asn Gly Glu Ala Asn Asn Lys Gly Gly Leu Glu  
405 410 415

Ala Val Leu Gly Val Glu Asp Phe Lys Phe Leu Val Asn Gly Glu Glu  
420 425 430

Gln Val Gly Glu Glu Lys Glu Gly Leu Asn Asn Gly Leu Asn Lys Leu  
435 440 445

Gly Ser Ser Ser Thr Val Glu Leu Gln Pro Lys Ala Thr Val Ala Gly  
450 455 460

Glu Ala Ser Ala Gly Lys His Met Pro Pro Ala Asn Val Met Thr Arg  
465 470 475 480

Leu Ile Leu Ile Met Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Thr  
485 490 495

Tyr Ser Ser Leu Ile Gly Val Val Trp Ser Leu Val Ala Phe Arg Trp  
500 505 510

His Val His Met Pro Lys Ile Ile Glu Lys Ser Ile Ser Ile Leu Ser  
515 520 525

Asp Ala Gly Leu Gly Met Ala Met Phe Ser Leu Gly  
530 535 540

<210> 27

<211> 525

<212> DNA

<213> Glycine max

<400> 27  
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caaaaaccaca tgctcttcca catccctata taaaatctt tcaatcttca taatcatcat 180  
catcaccacc aactccaact caaactctcc aaaacctgcc acttcaacct tcctatata 240  
tccttccctc actctcttct gcttctatca tctttctgag aggcttggg acacacaaaa 300  
aatgatcacc ttaacagact tctaccatgt gatgactgca atgggccac tctatgtggc 360  
catgatacta gcctatggct cagtgaaatg gtggaaagatt ttctccctg ataatgctct 420  
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tcaaacaacc ctatgaga tgaacctgaa ggtcctaact ggctg 525

<210> 28  
<211> 64  
<212> PRT  
<213> Glycine max

<220>  
<221> UNSURE  
<222> (38)

<400> 28  
Met Ile Thr Leu Thr Asp Phe Tyr His Val Met Thr Ala Met Val Pro  
1 5 10 15  
Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Lys Trp Trp Lys  
20 25 30  
Ile Phe Ser Pro Asp Xaa Cys Ser Gly Ile Asn Arg Phe Val Ala Leu  
35 40 45  
Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ala Ser Asn Asn Pro  
50 55 60

<210> 29  
<211> 2549  
<212> DNA  
<213> Glycine max

<400> 29  
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tcatcatcat caccaccaac tccaaactcaa actctccaaa acctgccact tcaaccttcc 240  
tatatatattcc tccctcaact ctcttctgtct tctatcatct ttctgagagg cttgttgaca 300  
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aatgctctgg catcaaccgt tttgtggcac tctttgcagt gcctttctc tccttccact 480  
tcatagcctc caacaaccct tatgagatga acctgagggtt cctagctgtct gacacccttc 540  
aaaagatcat aatactagtc ctccttgcag tttggagcaa catcaccaaa aggggttgg 600  
tggaatgggc cataacccttg ttctctctct ccaccctccc aaacactttt gttatggca 660  
tccctttgtct caaagggatg tatggtgact tctcaggag cctcatgggtt caaattgtgg 720  
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accctggcat gttctctccc tctaatgggt cccaaaagtgt tgctgcta at gcta at gccca 1320  
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 acttagttgtt tgaaaaaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 2520  
 aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 2549

&lt;210&gt; 30

&lt;211&gt; 605

&lt;212&gt; PRT

&lt;213&gt; Glycine max

&lt;400&gt; 30

Met	Ile	Thr	Leu	Thr	Asp	Phe	Tyr	His	Val	Met	Thr	Ala	Met	Val	Pro
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Leu	Tyr	Val	Ala	Met	Ile	Leu	Ala	Tyr	Gly	Ser	Val	Lys	Trp	Trp	Lys
										25				30	

Ile	Phe	Ser	Pro	Asp	Gln	Cys	Ser	Gly	Ile	Asn	Arg	Phe	Val	Ala	Leu
									35				40		45

Phe	Ala	Val	Pro	Leu	Leu	Ser	Phe	His	Ile	Ala	Ser	Asn	Asn	Pro	
									50				55		60

Tyr	Glu	Met	Asn	Leu	Arg	Phe	Leu	Ala	Ala	Asp	Thr	Leu	Gln	Lys	Ile	
										65				75		80

Ile	Ile	Leu	Val	Leu	Leu	Ala	Val	Trp	Ser	Asn	Ile	Thr	Lys	Arg	Gly
									85				90		95

Cys	Leu	Glu	Trp	Ala	Ile	Thr	Leu	Phe	Ser	Leu	Ser	Thr	Leu	Pro	Asn
									100				105		110

Thr	Leu	Val	Met	Gly	Ile	Pro	Leu	Leu	Lys	Gly	Met	Tyr	Gly	Asp	Phe
										115			120		125

Ser	Gly	Ser	Leu	Met	Val	Gln	Ile	Val	Val	Leu	Gln	Cys	Ile	Ile	Trp
										130			135		140

Tyr	Thr	Leu	Met	Leu	Phe	Leu	Phe	Glu	Phe	Arg	Gly	Ala	Arg	Met	Leu	
									145			150		155		160

Ile Ser Glu Gln Phe Pro Asp Thr Ala Ala Ser Ile Val Ser Ile His  
 165 170 175  
 Val Asp Ser Asp Val Met Ser Leu Asp Gly Arg Gln Pro Leu Glu Thr  
 180 185 190  
 Glu Ala Glu Ile Lys Glu Asp Gly Lys Leu His Val Thr Val Arg Lys  
 195 200 205  
 Ser Asn Ala Ser Arg Ser Asp Ile Phe Ser Arg Arg Ser Gln Gly Leu  
 210 215 220  
 Ser Ser Thr Thr Pro Arg Pro Ser Asn Leu Thr Asn Ala Glu Ile Tyr  
 225 230 235 240  
 Ser Leu Gln Ser Ser Arg Asn Pro Thr Pro Arg Gly Ser Ser Phe Asn  
 245 250 255  
 His Thr Asp Phe Tyr Ser Met Met Ala Ala Gly Gly Arg Asn Ser Asn  
 260 265 270  
 Phe Gly Ala Ser Asp Val Tyr Gly Leu Ser Ala Ser Arg Gly Pro Thr  
 275 280 285  
 Pro Arg Pro Ser Asn Tyr Asp Glu Asp Gly Gly Lys Pro Lys Phe His  
 290 295 300  
 Tyr His Ala Ala Gly Gly Thr Gly His Tyr Pro Ala Pro Asn Pro Gly  
 305 310 315 320  
 Met Phe Ser Pro Ser Asn Gly Ser Lys Ser Val Ala Ala Asn Ala Asn  
 325 330 335  
 Ala Lys Arg Pro Asn Gly Gln Ala Gln Leu Lys Pro Glu Asp Gly Asn  
 340 345 350  
 Arg Asp Leu His Met Phe Val Trp Ser Ser Ser Ala Ser Pro Val Ser  
 355 360 365  
 Asp Val Phe Gly Ala His Glu Tyr Gly Gly His Asp Gln Lys Glu  
 370 375 380  
 Val Lys Leu Asn Val Ser Pro Gly Lys Val Glu Asn Asn His Arg Asp  
 385 390 395 400  
 Thr Gln Glu Asp Tyr Leu Glu Lys Asp Glu Phe Ser Phe Gly Asn Arg  
 405 410 415  
 Glu Met Asp Arg Glu Met Asn Gln Leu Glu Gly Glu Lys Val Gly Asp  
 420 425 430  
 Gly Lys Pro Lys Thr Met Pro Pro Ala Ser Val Met Thr Arg Leu Ile  
 435 440 445  
 Leu Ile Met Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser  
 450 455 460  
 Ser Leu Ile Gly Leu Thr Trp Ser Leu Val Ser Phe Lys Trp Asn Val  
 465 470 475 480

Glu Met Pro Ala Ile Ile Ala Lys Ser Ile Ser Ile Leu Ser Asp Ala  
 485 490 495

Gly Leu Gly Met Ala Met Phe Ser Leu Gly Leu Phe Met Ala Leu Gln  
 500 505 510

Pro Arg Val Ile Ala Cys Gly Asn Ser Thr Ala Ala Phe Ala Met Ala  
 515 520 525

Val Arg Phe Leu Thr Gly Pro Ala Val Met Ala Ala Ala Ser Ile Ala  
 530 535 540

Val Gly Leu Lys Gly Val Leu Leu His Val Ala Ile Val Gln Ala Ala  
 545 550 555 560

Leu Pro Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Val  
 565 570 575

His Pro Asp Ile Leu Ser Thr Ala Val Ile Phe Gly Met Leu Ile Ala  
 580 585 590

Leu Pro Ile Thr Leu Val Tyr Tyr Ile Leu Leu Gly Leu  
 595 600 605

<210> 31

<211> 419

<212> DNA

<213> Glycine max

<220>

<221> unsure

<222> (237)

<220>

<221> unsure

<222> (250)

<220>

<221> unsure

<222> (347)

<400> 31

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 ctacatttgac ctagctagct acaaaaccctg cattaaccat gatcactggt aaggatattt 180  
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<210> 32

<211> 84

<212> PRT

<213> Glycine max

<220>

<221> UNSURE

<222> (25)

<220>  
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 <222> (32)

<220>  
 <221> UNSURE  
 <222> (64)

<400> 32

Met Ile Thr Gly Lys Asp Ile Tyr Asp Val Phe Ala Ala Ile Val Pro  
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Leu Tyr Val Ala Met Ile Leu Ser Xaa Tyr Gly Ser Val Arg Trp Xaa  
 20 25 30

Lys Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala  
 35 40 45

Val Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Ser Asn Xaa  
 50 55 60

Pro Tyr Ala Met Asn Tyr His Phe Ile Ala Ala Asp Cys Leu Gln Lys  
 65 70 75 80

Val Val Ile Leu

<210> 33  
 <211> 2324  
 <212> DNA  
 <213> Glycine max

<400> 33

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 gatattttagt atgttttcgc ggctattgtg cccctctacg ttgctatgat attagcatac 240  
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 aatagaaaaa gaagttatgt ttgctataac tgtacgtact atgtaaaccc aatgtcacgc 2160  
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&lt;210&gt; 34

&lt;211&gt; 637

&lt;212&gt; PRT

&lt;213&gt; Glycine max

&lt;400&gt; 34

Met	Ile	Thr	Gly	Lys	Asp	Ile	Tyr	Asp	Val	Phe	Ala	Ala	Ile	Val	Pro
1						5			10				15		

Leu	Tyr	Val	Ala	Met	Ile	Leu	Ala	Tyr	Gly	Ser	Val	Arg	Trp	Trp	Lys
					20				25				30		

Ile	Phe	Thr	Pro	Asp	Gln	Cys	Ser	Gly	Ile	Asn	Arg	Phe	Val	Ala	Val
					35			40				45			

Phe	Ala	Val	Pro	Leu	Leu	Ser	Phe	His	Phe	Ile	Ser	Ser	Asn	Asp	Pro
					50			55				60			

Tyr	Ala	Met	Asn	Tyr	His	Phe	Ile	Ala	Ala	Asp	Cys	Leu	Gln	Lys	Val
					65			70			75			80	

Val	Ile	Leu	Gly	Ala	Leu	Phe	Leu	Trp	Asn	Thr	Phe	Thr	Lys	His	Gly
					85				90				95		

Ser	Leu	Asp	Trp	Thr	Ile	Thr	Leu	Phe	Ser	Leu	Ser	Thr	Leu	Pro	Asn
					100				105				110		

Thr	Leu	Val	Met	Gly	Ile	Pro	Leu	Leu	Lys	Ala	Met	Tyr	Gly	Asp	Phe
					115			120				125			

Ser	Gly	Ser	Leu	Met	Val	Gln	Ile	Val	Val	Leu	Gln	Ser	Val	Ile	Trp
					130			135			140				

Tyr	Thr	Leu	Met	Leu	Phe	Met	Phe	Glu	Tyr	Arg	Gly	Ala	Lys	Leu	Leu
					145			150			155			160	

Ile	Thr	Glu	Gln	Phe	Pro	Glu	Thr	Ala	Gly	Ser	Ile	Thr	Ser	Phe	Arg
					165				170				175		

Val	Asp	Ser	Asp	Val	Val	Ser	Leu	Asn	Gly	Arg	Glu	Pro	Leu	Gln	Thr
					180			185				190			

Asp	Ala	Glu	Ile	Gly	Glu	Asp	Gly	Lys	Leu	His	Val	Val	Val	Lys	Arg
					195			200				205			

Ser	Ala	Ala	Ser	Ser	Met	Ile	Ser	Ser	Phe	Asn	Lys	Ser	His	Leu	Thr
					210			215			220				

Ser Met Thr Pro Arg Ala Ser Asn Leu Thr Gly Val Glu Ile Tyr Ser  
225 230 235 240

Val Gln Ser Ser Arg Glu Pro Thr Pro Arg Gly Ser Ser Phe Asn Gln  
245 250 255

Thr Asp Phe Tyr Ala Met Phe Ala Ser Lys Ala Pro Ser Pro Lys His  
260 265 270

Gly Tyr Thr Asn Ser Phe Gln Ser Asn Asn Gly Gly Ile Gly Asp Val  
275 280 285

Tyr Ser Leu Gln Ser Ser Lys Gly Ala Thr Pro Arg Thr Ser Asn Phe  
290 295 300

Glu Glu Glu Met Leu Lys Met His Lys Lys Arg Gly Gly Arg Ser Met  
305 310 315 320

Ser Gly Glu Leu Phe Asn Gly Gly Leu Val Ser Ser Asn Tyr Pro Pro  
325 330 335

Pro Asn Pro Met Phe Ser Gly Ser Thr Ser Ala Ala Gly Gly Pro Lys  
340 345 350

Lys Lys Asp Ser Ser Gly Gly Gly Ala Val Ala Pro Asn Lys Glu  
355 360 365

Leu His Met Phe Val Trp Ser Ser Ser Ala Ser Pro Val Ser Glu Gly  
370 375 380

Asn Leu Arg His Ala Val Asn Arg Ala Ala Ser Thr Asp Phe Gly Thr  
385 390 395 400

Val Asp Pro Ser Lys Ala Val Pro His Glu Thr Val Ala Ser Lys Ala  
405 410 415

Val His Glu Leu Ile Glu Asn Met Ser Pro Gly Arg Arg Gly Ser Gly  
420 425 430

Glu Arg Glu Pro Glu Met Asp Glu Gly Ala Lys Ile Pro Ala Ser Gly  
435 440 445

Ser Pro Tyr Thr Cys Gln Lys Lys Val Asp Met Glu Asp Gly Asn Ala  
450 455 460

Asn Lys Asn Gln Gln Met Pro Pro Ala Ser Val Met Thr Arg Leu Ile  
465 470 475 480

Leu Ile Met Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser  
485 490 495

Ser Leu Leu Gly Leu Thr Trp Ser Leu Ile Ser Phe Arg Trp His Ile  
500 505 510

Glu Met Pro Thr Ile Val Lys Gly Ser Ile Ser Ile Leu Ser Asp Ala  
515 520 525

Gly Leu Gly Met Ala Met Phe Ser Leu Gly Leu Phe Met Ala Leu Gln  
530 535 540

Pro Lys Ile Ile Ala Cys Gly Lys Ser Val Ala Ala Phe Ser Met Ala  
545 550 555 560

Val Arg Phe Leu Thr Gly Pro Ala Val Ile Ala Ala Thr Ser Ile Gly  
565 570 575

Ile Gly Leu Arg Gly Val Leu Leu His Val Ala Ile Val Gln Ala Ala  
580 585 590

Leu Pro Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Leu  
595 600 605

His Ala Asp Ile Leu Ser Thr Ala Val Ile Phe Gly Met Leu Ile Ala  
610 615 620

Leu Pro Ile Thr Ile Leu Tyr Tyr Val Leu Leu Gly Val  
625 630 635

<210> 35  
<211> 473  
<212> DNA  
<213> Triticum aestivum

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<222> (441)

<400> 35  
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ncgatgatta cccggaaggc catctaccac ntgctggngg nggtggtgcc gctgtacgtg 120  
gncatgttca tggcgtacgg gtcggcgcgg tggtgggca tcttacgccc ggaccantgc 180  
tcgggcatca aacgcttcgt ngccgtcttc gccgtggcgc tcctctcctt ccacttcatc 240  
tccaccaacg aaccctacgc catgactaa cgcttcctgg gcccggactc gctgcanaan 300  
ntcgatatcc tcgcccgcct cggcgtgtgg ganaangtgc tctcccncca acgggtgccc 360

ggggganaga aggccggcgaa ggctcctcnc tgggctggga caacanactc ttctccttgg 420  
ggaaagtgcc aaaanactgg ngaaggggaa tccccctgct gggcgcaagt atg 473

<210> 36  
<211> 89  
<212> PRT  
<213> *Triticum aestivum*

<220>  
<221> UNSURE  
<222> (10)

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<222> (12)...(13) .

<220>  
<221> UNSURE  
<222> (20)

<220>  
<221> UNSURE  
<222> (38)

<220>  
<221> UNSURE  
<222> (69)

<220>  
<221> UNSURE  
<222> (78)...(79)...(80)

<220>  
<221> UNSURE  
<222> (85)

<400> 36  
Met Ile Thr Gly Lys Asp Ile Tyr His Xaa Leu Xaa Xaa Val Val Pro  
1 5 10 15

Leu Tyr Val Xaa Met Phe Met Ala Tyr Gly Ser Val Arg Trp Trp Gly  
20 25 30

Ile Phe Thr Pro Asp Xaa Cys Ser Gly Ile Lys Arg Phe Val Ala Val  
35 40 45

Phe Ala Val Ala Leu Leu Ser Phe His Phe Ile Ser Thr Asn Glu Pro  
50 55 60

Tyr Ala Met Asp Xaa Arg Phe Leu Gly Ala Asp Ser Leu Xaa Xaa Xaa  
65 70 75 80

Val Ile Leu Ala Xaa Leu Ala Val Trp  
85

<210> 37  
<211> 2293  
<212> DNA  
<213> *Triticum aestivum*

&lt;400&gt; 37

ctggatcgat ccccagcagc agagacgaga tcccacgagg aaccgttggg atctagctag 60  
 ctagctcgac gcgatgatca ccgggaagga catctacgac gtgctggcgg cggtggtgc 120  
 gctgtacgtg gccatgttca tggctacgg gtcgggtcgg tggtggggca tcttacacgc 180  
 ggaccagtgc tcgggcataca accgccttcgt cgccgtcttc gcgggtccgc tccttcctt 240  
 ccacttcatac tccaccaacg acccctacgc catggactac cgcttcctgg cgcccgactc 300  
 gctgcagaag ctcgtcatcc tcgcccgcct cgccgtgtgg cacaacgtgc tctccgcta 360  
 ccggtgcgcg ggcggcacgg aggccggcga ggcctcgctg ctggacttgg aacatcacgc 420  
 ctctccctg gcgacgctgc ccaacacgc ggtgatgggc atcccgctgc tgccgcgc 480  
 gtacggcgcac ttctcggggt cgctcatggc gcagatcgat gtgctgcaga gcgtcatctg 540  
 gtacacgcctc atgcttc tcttcgagta cccggcgc aaggcgctca tctccgagca 600  
 gttccgcggc gacgtcgccg ccagcatcgcc ctccctccgc gtcgactccg acgtcgctc 660  
 gctcaacggg cgcgaggcgc tgcaagccga cgccgaggc ggcgcgcac gccgcgtcca 720  
 cgtcgatccatc cgccgggtccg cgtcgggtc caccacggc ggcacacggc ccgggcgc 780  
 cgggatctac cgtggcgcgt ccaacgcac gacggcgc gcttcaacc tcacgggcgt 840  
 ggagatctac tcgctgcaga cgtcgggca gcccacgcg aggcaatcca gtttcaacca 900  
 gtccgacttc tactccatgt tcaacgggag caagctggct agtcccaagg gccagcccc 960  
 cgtcgccggc ggtgggtggc cgcggggca ggggctcgac gaggcagggtgg ccaacaagtt 1020  
 caaggcgcc gaggcggtcg cgcctaccc cgcggccaaac cccggatgt tgatgccgc 1080  
 gccacggaa aaggagctt ggggttccaa ctcaaaactcg aacaaggagc tgacatgtt 1140  
 cgtgtggagc tccagcgcgt cgcggcgtc ggaggccaaac ctccgcacac cggttcaacca 1200  
 cgcgcgtcc accgacttc cgcggcgcacc gccggcggca gccacgcac gagacggcgc 1260  
 cacaccaga ggcgtgagcg gcagcgtgac gccgggtatg aagaaggacg ccagcagcgg 1320  
 cgcgggtggag gtggagatcg aggacggcat gatgaagagc cggcgacgg ggctgggcgc 1380  
 caagttcccg gtgtcggtt cccctacgt ggccccggc aagaaggcg cgcgttgc 1440  
 tgggctggag gaggcgccg acccgatgcc gccggcggc gttatgacc ggcttcatcct 1500  
 catcatggtg tggcgcaagc tcatccgc ccccaacacc tactccagcc tcattccgc 1560  
 cgtctggta ctcgtctc tcaagttggaa cattcagatg ctttacaataa tcaaggggtc 1620  
 catatccatc ctgtctgtatc caggctagg gatggctatg ttcagcttag gtctttcat 1680  
 ggctctgcaa ccaaagatca tctttgcgg gaagtctgtc gccacattt caatggcagt 1740  
 gaggttctt gactggccgg cgggtatcg cgcgacccatca atcggccgtcg ggctccgggg 1800  
 agtgcttcta catgttgc cttgtccaggc agcaatcca caaggaattt ttccattttgt 1860  
 gttcgccaag gactacaatt gccatctca aatacttagc acagcggtt tttttggat 1920  
 gctcggtgc ctcccgatca cgataactcta ctacgttctc ctggatat agattataa 1980  
 tcttgaagaa ccaaggctgc aaatcttcgg gtagggagaa gtagaaatttct agagagaaaa 2040  
 tggcaactga acatgttgc gggctgtcct gaagacctga agatgcatga gaccaagcag 2100  
 aaggataggg agaactaagt aggaccctag acaggaattt aaaggacaga taaagatatac 2160  
 cttgggttcca ttttttaat tttttatatt atttttacta ctgttttaga tccaaagtaa 2220  
 aggcttagggc ttttagtataa aagagttcaa ccgtttaatc gaaaaaaaaaaaaaaa 2280  
 aaaaaaaaaaaa aaa 2293

&lt;210&gt; 38

&lt;211&gt; 632

&lt;212&gt; PRT

&lt;213&gt; Triticum aestivum

&lt;400&gt; 38

Met	Ile	Thr	Gly	Lys	Asp	Ile	Tyr	Asp	Val	Leu	Ala	Ala	Val	Val	Pro
1									10					15	

Leu	Tyr	Val	Ala	Met	Phe	Met	Ala	Tyr	Gly	Ser	Val	Arg	Trp	Trp	Gly
										20				30	

Ile	Phe	Thr	Pro	Asp	Gln	Cys	Ser	Gly	Ile	Asn	Arg	Phe	Val	Ala	Val
									35				40		45

Phe	Ala	Val	Pro	Leu	Leu	Ser	Phe	His	Phe	Ile	Ser	Thr	Asn	Asp	Pro
									50				55		60

Tyr Ala Met Asp Tyr Arg Phe Leu Ala Ala Asp Ser Leu Gln Lys Leu  
65 70 75 80

Val Ile Leu Ala Ala Leu Ala Val Trp His Asn Val Leu Ser Arg Tyr  
85 90 95

Arg Cys Arg Gly Gly Thr Glu Ala Gly Glu Ala Ser Ser Leu Asp Trp  
100 105 110

Thr Ile Thr Leu Phe Ser Leu Ala Thr Leu Pro Asn Thr Leu Val Met  
115 120 125

Gly Ile Pro Leu Leu Arg Ala Met Tyr Gly Asp Phe Ser Gly Ser Leu  
130 135 140

Met Val Gln Ile Val Val Leu Gln Ser Val Ile Trp Tyr Thr Leu Met  
145 150 155 160

Leu Phe Leu Phe Glu Tyr Arg Gly Ala Lys Ala Leu Ile Ser Glu Gln  
165 170 175

Phe Pro Pro Asp Val Gly Ala Ser Ile Ala Ser Phe Arg Val Asp Ser  
180 185 190

Asp Val Val Ser Leu Asn Gly Arg Glu Ala Leu His Ala Asp Ala Glu  
195 200 205

Val Gly Arg Asp Gly Arg Val His Val Val Ile Arg Arg Ser Ala Ser  
210 215 220

Gly Ser Thr Thr Gly Gly His Gly Ala Gly Arg Ser Gly Ile Tyr Arg  
225 230 235 240

Gly Ala Ser Asn Ala Met Thr Pro Arg Ala Ser Asn Leu Thr Gly Val  
245 250 255

Glu Ile Tyr Ser Leu Gln Thr Ser Arg Glu Pro Thr Pro Arg Gln Ser  
260 265 270

Ser Phe Asn Gln Ser Asp Phe Tyr Ser Met Phe Asn Gly Ser Lys Leu  
275 280 285

Ala Ser Pro Lys Gly Gln Pro Pro Val Ala Gly Gly Gly Ala Arg  
290 295 300

Gly Gln Gly Leu Asp Glu Gln Val Ala Asn Lys Phe Lys Gly Gly Glu  
305 310 315 320

Ala Ala Ala Pro Tyr Pro Ala Pro Asn Pro Gly Met Met Met Pro Ala  
325 330 335

Pro Arg Lys Lys Glu Leu Gly Gly Ser Asn Ser Asn Ser Asp Lys Glu  
340 345 350

Leu His Met Phe Val Trp Ser Ser Ser Ala Ser Pro Val Ser Glu Ala  
355 360 365

Asn Leu Arg Asn Ala Val Asn His Ala Ala Ser Thr Asp Phe Ala Ala  
370 375 380

Ala Pro Pro Ala Ala Ala Thr Pro Arg Asp Gly Ala Thr Pro Arg Gly  
385 390 395 400

Val Ser Gly Ser Val Thr Pro Val Met Lys Lys Asp Ala Ser Ser Gly  
405 410 415

Ala Val Glu Val Glu Ile Glu Asp Gly Met Met Lys Ser Pro Ala Thr  
420 425 430

Gly Leu Gly Ala Lys Phe Pro Val Ser Gly Ser Pro Tyr Val Ala Pro  
435 440 445

Arg Lys Lys Gly Ala Asp Val Pro Gly Leu Glu Glu Ala Ala His Pro  
450 455 460

Met Pro Pro Ala Ser Val Met Thr Arg Leu Ile Leu Ile Met Val Trp  
465 470 475 480

Arg Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser Ser Leu Ile Gly Leu  
485 490 495

Val Trp Ser Leu Val Ser Phe Arg Trp Asn Ile Gln Met Pro Thr Ile  
500 505 510

Ile Lys Gly Ser Ile Ser Ile Leu Ser Asp Ala Gly Leu Gly Met Ala  
515 520 525

Met Phe Ser Leu Gly Leu Phe Met Ala Leu Gln Pro Lys Ile Ile Ser  
530 535 540

Cys Gly Lys Ser Val Ala Thr Phe Ala Met Ala Val Arg Phe Leu Thr  
545 550 555 560

Gly Pro Ala Val Ile Ala Ala Thr Ser Ile Ala Val Gly Leu Arg Gly  
565 570 575

Val Leu Leu His Val Ala Ile Val Gln Ala Ala Leu Pro Gln Gly Ile  
580 585 590

Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Cys His Pro Gln Ile Leu  
595 600 605

Ser Thr Ala Val Ile Phe Gly Met Leu Val Ala Leu Pro Ile Thr Ile  
610 615 620

Leu Tyr Tyr Val Leu Leu Gly Ile  
625 630

<210> 39  
<211> 447  
<212> DNA  
<213> Triticum aestivum

<220>  
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<222> (366)

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<221> unsure  
<222> (380)

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<221> unsure  
<222> (418)

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<222> (421)

<220>  
<221> unsure  
<222> (434)

<400> 39  
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aagggtgtgg aggcgatggc gcccgtttac ttgcgtctag ggctcggtt cgggtccgtt 120  
cgatgggtggc ggttcttac ggcggagcag tgcggcgcca tcaacacgct ggtggtctgc 180  
ttctccatgc ccttcttac cttcgacttc gtggtcccgcc cggaccccta cgccatgaat 240  
taccgcgtca tcgcccggca cggcgtcgcc aaacttctcg cggcgctcgcc cggccgcgtc 300  
tgggcgcgtt gcgccaaggc caaggccggc gcctactcgt ggtcatcacg gggttctccc 360  
tgggcncgtt caacaacacn ctcgtcgtn gggtgccgtt tctgggacgc caatttcngg 420  
naattggggg gcaangactt tattttt 447

<210> 40  
<211> 94  
<212> PRT  
<213> Triticum aestivum

<400> 40  
Met Ile Ala Leu Gly Asp Ile Tyr Lys Val Val Glu Ala Met Ala Pro  
1 5 10 15

Leu Tyr Phe Ala Leu Gly Leu Gly Tyr Gly Ser Val Arg Trp Trp Arg  
20 25 30

Phe Phe Thr Ala Glu Gln Cys Gly Ala Ile Asn Thr Leu Val Val Cys  
35 40 45

Phe Ser Met Pro Phe Phe Thr Phe Asp Phe Val Val Arg Ala Asp Pro  
50 55 60

Tyr Ala Met Asn Tyr Arg Val Ile Ala Ala Asp Ala Val Ala Lys Leu  
65 70 75 80

Leu Ala Val Leu Ala Ala Val Trp Ala Arg Cys Ala Lys  
85 90

<210> 41  
<211> 415  
<212> DNA  
<213> Triticum aestivum

<400> 41  
ctcgcttaaa taaacctctc ccccaacgcac tccccactc caccacacac cctcaccaggc 60  
tcgcccgcag agtgagccga ggccgagagc cggagcgcga gaggaagaag cagaggaggt 120  
cgggcaagat gatcacgggc acggacttct accacgtgtat gacggcggtg gtggcgctgt 180

acgtggccat gatcctcgcc tacggctccg tcaagtggtg gggcatcttc acgcccggacc 240  
 atgctccgg gatcaaccgc ttcgtcgcc tcttcgcgt gccgccttc tccttccact 300  
 tcatactccac caacaacccc tacaccatga acctgcgcctt catgcggcc gacacgctgc 360  
 agaagctcat gatgctcgcc atgctcaacg cctggagcaa ctctcccgcc gcggc 415

<210> 42  
 <211> 91  
 <212> PRT  
 <213> *Triticum aestivum*

<400> 42  
 Met Ile Thr Gly Thr Asp Phe Tyr His Val Met Thr Ala Val Val Pro  
 1 5 10 15

Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Lys Trp Trp Gly  
 20 25 30

Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Leu  
 35 40 45

Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asn Pro  
 50 55 60

Tyr Thr Met Asn Leu Arg Phe Ile Ala Ala Asp Thr Leu Gln Lys Leu  
 65 70 75 80

Met Met Leu Ala Met Leu Asn Ala Trp Ser Asn  
 85 90

<210> 43  
 <211> 647  
 <212> PRT  
 <213> *Arabidopsis thaliana*

<400> 43  
 Met Ile Thr Gly Lys Asp Met Tyr Asp Val Leu Ala Ala Met Val Pro  
 1 5 10 15

Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Arg Trp Trp Gly  
 20 25 30

Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Val  
 35 40 45

Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Ser Asn Asp Pro  
 50 55 60

Tyr Ala Met Asn Tyr His Phe Leu Ala Ala Asp Ser Leu Gln Lys Val  
 65 70 75 80

Val Ile Leu Ala Ala Leu Phe Leu Trp Gln Ala Phe Ser Arg Arg Gly  
 85 90 95

Ser Leu Glu Trp Met Ile Thr Leu Phe Ser Leu Ser Thr Leu Pro Asn  
 100 105 110

Thr Leu Val Met Gly Ile Pro Leu Leu Arg Ala Met Tyr Gly Asp Phe  
 115 120 125

Ser Gly Asn Leu Met Val Gln Ile Val Val Leu Gln Ser Ile Ile Trp  
130 135 140

Tyr Thr Leu Met Leu Phe Leu Phe Glu Phe Arg Gly Ala Lys Leu Leu  
145 150 155 160

Ile Ser Glu Gln Phe Pro Glu Thr Ala Gly Ser Ile Thr Ser Phe Arg  
165 170 175

Val Asp Ser Asp Val Ile Ser Leu Asn Gly Arg Glu Pro Leu Gln Thr  
180 185 190

Asp Ala Glu Ile Gly Asp Asp Gly Lys Leu His Val Val Val Arg Arg  
195 200 205

Ser Ser Ala Ala Ser Ser Met Ile Ser Ser Phe Asn Lys Ser His Gly  
210 215 220

Gly Gly Leu Asn Ser Ser Met Ile Thr Pro Arg Ala Ser Asn Leu Thr  
225 230 235 240

Gly Val Glu Ile Tyr Ser Val Gln Ser Ser Arg Glu Pro Thr Pro Arg  
245 250 255

Ala Ser Ser Phe Asn Gln Thr Asp Phe Tyr Ala Met Phe Asn Ala Ser  
260 265 270

Lys Ala Pro Ser Pro Arg His Gly Tyr Thr Asn Ser Tyr Gly Gly Ala  
275 280 285

Gly Ala Gly Pro Gly Gly Asp Val Tyr Ser Leu Gln Ser Ser Lys Gly  
290 295 300

Val Thr Pro Arg Thr Ser Asn Phe Asp Glu Glu Val Met Lys Thr Ala  
305 310 315 320

Lys Lys Ala Gly Arg Gly Arg Ser Met Ser Gly Glu Leu Tyr Asn  
325 330 335

Asn Asn Ser Val Pro Ser Tyr Pro Pro Asn Pro Met Phe Thr Gly  
340 345 350

Ser Thr Ser Gly Ala Ser Gly Val Lys Lys Lys Glu Ser Gly Gly Gly  
355 360 365

Gly Ser Gly Gly Gly Val Gly Val Gly Gly Gln Asn Lys Glu Met Asn  
370 375 380

Met Phe Val Trp Ser Ser Ser Ala Ser Pro Val Ser Glu Ala Asn Ala  
385 390 395 400

Lys Asn Ala Met Thr Arg Gly Ser Ser Thr Asp Val Ser Thr Asp Pro  
405 410 415

Lys Val Ser Ile Pro Pro His Asp Asn Leu Ala Thr Lys Ala Met Gln  
420 425 430

Asn Leu Ile Glu Asn Met Ser Pro Gly Arg Lys Gly His Val Glu Met  
435 440 445

Asp Gln Asp Gly Asn Asn Gly Gly Lys Ser Pro Tyr Met Gly Lys Lys  
 450 455 460

Gly Ser Asp Val Glu Asp Gly Gly Pro Gly Pro Arg Lys Gln Gln Met  
 465 470 475 480

Pro Pro Ala Ser Val Met Thr Arg Leu Ile Leu Ile Met Val Trp Arg  
 485 490 495

Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser Ser Leu Phe Gly Leu Ala  
 500 505 510

Trp Ser Leu Val Ser Phe Lys Trp Asn Ile Lys Met Pro Thr Ile Met  
 515 520 525

Ser Gly Ser Ile Ser Ile Leu Ser Asp Ala Gly Leu Gly Met Ala Met  
 530 535 540

Phe Ser Leu Gly Leu Phe Met Ala Leu Gln Pro Lys Ile Ile Ala Cys  
 545 550 555 560

Gly Lys Ser Val Ala Gly Phe Ala Met Ala Val Arg Phe Leu Thr Gly  
 565 570 575

Pro Ala Val Ile Ala Ala Thr Ser Ile Ala Ile Gly Ile Arg Gly Asp  
 580 585 590

Leu Leu His Ile Ala Ile Val Gln Ala Ala Leu Pro Gln Gly Ile Val  
 595 600 605

Pro Phe Val Phe Ala Lys Glu Tyr Asn Val His Pro Asp Ile Leu Ser  
 610 615 620

Thr Ala Val Ile Phe Gly Met Leu Val Ala Leu Pro Val Thr Val Leu  
 625 630 635 640

Tyr Tyr Val Leu Leu Gly Leu  
 645

<210> 44  
 <211> 622  
 <212> PRT  
 <213> *Arabidopsis thaliana*

<400> 44  
 Met Ile Thr Ala Ala Asp Phe Tyr His Val Met Thr Ala Met Val Pro  
 1 5 10 15

Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Lys Trp Trp Lys  
 20 25 30

Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Leu  
 35 40 45

Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ala Ala Asn Asn Pro  
 50 55 60

Tyr Ala Met Asn Leu Arg Phe Leu Ala Ala Asp Ser Leu Gln Lys Val  
 65 70 75 80

Ile Val Leu Ser Leu Leu Phe Leu Trp Cys Lys Leu Ser Arg Asn Gly  
85 90 95

Ser Leu Asp Trp Thr Ile Thr Leu Phe Ser Leu Ser Thr Leu Pro Asn  
100 105 110

Thr Leu Val Met Gly Ile Pro Leu Leu Lys Gly Met Tyr Gly Asn Phe  
115 120 125

Ser Gly Asp Leu Met Val Gln Ile Val Val Leu Gln Cys Ile Ile Trp  
130 135 140

Tyr Ile Leu Met Leu Phe Leu Phe Glu Tyr Arg Gly Ala Lys Leu Leu  
145 150 155 160

Ile Ser Glu Gln Phe Pro Asp Thr Ala Gly Ser Ile Val Ser Ile His  
165 170 175

Val Asp Ser Asp Ile Met Ser Leu Asp Gly Arg Gln Pro Leu Glu Thr  
180 185 190

Glu Ala Glu Ile Lys Glu Asp Gly Lys Leu His Val Thr Val Arg Arg  
195 200 205

Ser Asn Ala Ser Arg Ser Asp Ile Tyr Ser Arg Arg Ser Gln Gly Leu  
210 215 220

Ser Ala Thr Pro Arg Pro Ser Asn Leu Thr Asn Ala Glu Ile Tyr Ser  
225 230 235 240

Leu Gln Ser Ser Arg Asn Pro Thr Pro Arg Gly Ser Ser Phe Asn His  
245 250 255

Thr Asp Phe Tyr Ser Met Met Ala Ser Gly Gly Arg Asn Ser Asn  
260 265 270

Phe Gly Pro Gly Glu Ala Val Phe Gly Ser Lys Gly Pro Thr Pro Arg  
275 280 285

Pro Ser Asn Tyr Glu Glu Asp Gly Gly Pro Ala Lys Pro Thr Ala Ala  
290 295 300

Gly Thr Ala Ala Gly Ala Gly Arg Phe His Tyr Gln Ser Gly Gly Ser  
305 310 315 320

Gly Gly Gly Gly Ala His Tyr Pro Ala Pro Asn Pro Gly Met Phe  
325 330 335

Ser Pro Asn Thr Gly Gly Gly Gly Thr Ala Ala Lys Gly Asn Ala  
340 345 350

Pro Val Val Gly Gly Lys Arg Gln Asp Gly Asn Gly Arg Asp Leu His  
355 360 365

Met Phe Val Trp Ser Ser Ala Ser Pro Val Ser Asp Val Phe Gly  
370 375 380

Gly Gly Gly Gly Asn His His Ala Asp Tyr Ser Thr Ala Thr Asn Asp  
385 390 395 400

His Gln Lys Asp Val Lys Ile Ser Val Pro Gln Gly Asn Ser Asn Asp  
405 410 415

Asn Gln Tyr Val Glu Arg Glu Glu Phe Ser Phe Gly Asn Lys Asp Asp  
420 425 430

Asp Ser Lys Val Leu Ala Thr Asp Gly Gly Asn Asn Ile Ser Asn Lys  
435 440 445

Thr Thr Gln Ala Lys Val Met Pro Pro Thr Ser Val Met Thr Arg Leu  
450 455 460

Ile Leu Ile Met Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Ser Tyr  
465 470 475 480

Ser Ser Leu Phe Gly Ile Thr Trp Ser Leu Ile Ser Phe Lys Trp Asn  
485 490 495

Ile Glu Met Pro Ala Leu Ile Ala Lys Ser Ile Ser Ile Leu Ser Asp  
500 505 510

Ala Gly Leu Gly Met Ala Met Phe Ser Leu Gly Leu Phe Met Ala Leu  
515 520 525

Asn Pro Arg Ile Ile Ala Cys Gly Asn Arg Arg Ala Ala Phe Ala Ala  
530 535 540

Ala Met Arg Phe Val Val Gly Pro Ala Val Met Leu Val Ala Ser Tyr  
545 550 555 560

Ala Val Gly Leu Arg Gly Val Leu Leu His Val Ala Ile Ile Gln Ala  
565 570 575

Ala Leu Pro Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn  
580 585 590

Val His Pro Asp Ile Leu Ser Thr Ala Val Ile Phe Gly Met Leu Ile  
595 600 605

Ala Leu Pro Ile Thr Leu Leu Tyr Tyr Ile Leu Leu Gly Leu  
610 615 620

<210> 45

<211> 425

<212> DNA

<213> *Triticum aestivum*

<400> 45

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caccagctcg cccgcagagt gagccgagc cgagagccgg agcgcgagag gaagaagcag 120  
aggaggtcgg gcaagatgtat cacgggcacg gacttctacc acgtgatgac ggccgtgggt 180  
ccgctgtacg tggccatgtat cctcgctac ggctccgtca agtgggtgggg catcttcacg 240  
ccggaccagt gctccggat caaccgcttc gtcgcgtct tcggcgtgcc gtcctctcc 300  
ttccacttca tctccaccaa caaccctac accatgaacc tgcgcttcat cgccgcccac 360  
acgctgcaga agctcatgt gtcgcccgt ctcaccgcct ggagccacct ctcccggccgc 420  
ggcag 425

<210> 46

<211> 96

&lt;212&gt; PRT

&lt;213&gt; Triticum aestivum

&lt;400&gt; 46

Met	Ile	Thr	Gly	Thr	Asp	Phe	Tyr	His	Val	Met	Thr	Ala	Val	Val	Pro
1						5			10					15	

Leu	Tyr	Val	Ala	Met	Ile	Leu	Ala	Tyr	Gly	Ser	Val	Lys	Trp	Trp	Gly
					20			25				30			

Ile	Phe	Thr	Pro	Asp	Gln	Cys	Ser	Gly	Ile	Asn	Arg	Phe	Val	Ala	Leu
					35			40			45				

Phe	Ala	Val	Pro	Leu	Leu	Ser	Phe	His	Phe	Ile	Ser	Thr	Asn	Asn	Pro
					50			55			60				

Tyr	Thr	Met	Asn	Leu	Arg	Phe	Ile	Ala	Ala	Asp	Thr	Leu	Gln	Lys	Leu
					65			70			75		80		

Met	Met	Leu	Ala	Met	Leu	Thr	Ala	Trp	Ser	His	Leu	Ser	Arg	Arg	Gly
					85			90				95			

&lt;210&gt; 47

&lt;211&gt; 855

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;400&gt; 47

ccacgcgtcc	ggctgatcgt	cctggcgctg	ctcactgcat	ggagctaccc	ctccgcgg	60
ggctgcctcg	agtggaccat	cacgctttc	tccctgtcga	cgctgccaa	cacgctgg	120
atgggcatcc	cgctgctcaa	gggcatgtac	ggcgacttct	ccggcagcct	catggtgcag	180
atcgtggtgc	tccagtgc	catctggtac	acgctgatgc	tgttcatgtt	cgagtaccgc	240
ggcgccagga	tcctcatcac	cgagcagttc	cccgacacgg	cgggcgccat	cgcctccatc	300
gtggtggacc	ccgacgttgt	gtcgctggac	gggchgcaacg	acggccatcga	gacggaggcc	360
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accaacgccc	agatctactc	gctcgagtcg	tcgagggaaacc	ccacgcccgc	gggctccagc	540
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gcgttccggcc	tgcgcacggg	cgccacgccc	aggccgtcca	actacgagga	ggacccgcag	660
ggcaaggcga	acaagtacgg	ccagtagccg	gcccacaacc	cgcccatggc	ggcgccagccc	720
gccaaggggcc	tcaagaaggc	ggccaatggg	caggccaagg	gcaaggacgg	caaggaccta	780
cacatgttcg	tgtggagctc	cagcgcgtcg	cccggttccg	acgtgttccg	aatggcgcc	840
gccgagataca	acgac					855

&lt;210&gt; 48

&lt;211&gt; 285

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;400&gt; 48

Pro	Arg	Val	Arg	Leu	Ile	Val	Leu	Ala	Leu	Leu	Thr	Ala	Trp	Ser	Tyr
1					5			10			15				

Leu	Ser	Arg	Arg	Gly	Cys	Leu	Glu	Trp	Thr	Ile	Thr	Leu	Phe	Ser	Leu
					20			25			30				

Ser	Thr	Leu	Pro	Asn	Thr	Leu	Val	Met	Gly	Ile	Pro	Leu	Leu	Lys	Gly
					35			40			45				

Met Tyr Gly Asp Phe Ser Gly Ser Leu Met Val Gln Ile Val Val Leu  
50 55 60

Gln Cys Ile Ile Trp Tyr Thr Leu Met Leu Phe Met Phe Glu Tyr Arg  
65 70 75 80

Gly Ala Arg Ile Leu Ile Thr Glu Gln Phe Pro Asp Thr Ala Gly Ala  
85 90 95

Ile Ala Ser Ile Val Val Asp Pro Asp Val Val Ser Leu Asp Gly Arg  
100 105 110

Asn Asp Ala Ile Glu Thr Glu Ala Glu Val Lys Glu Asp Gly Lys Ile  
115 120 125

His Val Thr Val Arg Arg Ser Asn Ala Ser Arg Ser Asp Ile Tyr Ser  
130 135 140

Arg Arg Ser Met Gly Phe Ser Ser Thr Thr Pro Arg Pro Ser Asn Leu  
145 150 155 160

Thr Asn Ala Glu Ile Tyr Ser Leu Gln Ser Ser Arg Asn Pro Thr Pro  
165 170 175

Arg Gly Ser Ser Phe Asn His Thr Asp Phe Tyr Ser Met Val Gly Arg  
180 185 190

Ser Ser Asn Phe Ala Ala Gly Asp Ala Phe Gly Leu Arg Thr Gly Ala  
195 200 205

Thr Pro Arg Pro Ser Asn Tyr Glu Glu Asp Pro Gln Gly Lys Ala Asn  
210 215 220

Lys Tyr Gly Gln Tyr Pro Ala Pro Asn Pro Ala Met Ala Ala Gln Pro  
225 230 235 240

Ala Lys Gly Leu Lys Lys Ala Ala Asn Gly Gln Ala Lys Gly Glu Asp  
245 250 255

Gly Lys Asp Leu His Met Phe Val Trp Ser Ser Ser Ala Ser Pro Val  
260 265 270

Ser Asp Val Phe Gly Asn Gly Ala Ala Glu Tyr Asn Asp  
275 280 285